Promoter 01

-1161 CACAAACATA CACTCAAAAT CCAGACTCAC ATCTACTCAA TTATGCAACT
-1111 TCATCATGAA AACATCAAAA ACAGTCAAAG TAACAAAATC AAGTCAGATT
-1061 CAGCACACAA AGCCAGTAAA GATAGAAAAT TTAACGAACG CTCATGCTAA
-1011 GCTGCGCAAA ATACTTCCTA ATCAAAACAG TAACAACGAG TAATTAGCAA
- 961 AATCCGAGCA GAAAACTCTC ACCCACCTCC GAAATTCACG TCTTCACTAA
- 911 AATTTTCGAA AGGAATCGAT CAATACCAAC CCATTACACA AAATACATAA
- 861 TCAAAATGGC GAGAATCGTA CCTGGAAACT TTGCTTCAAG TCGCAGAGAG
- 811 AGGAAAAGGA AGATCGTGGA GAAAGGGGTT TAGGGTTTAA GCTCAGACTT
- 761 CTATTGGAGT AAATGGGACG GTGTCACATT TTCCGTTTTG GAAATGAACT
- 711 TTGGGCTCAC GTTATGGGCT ATTAGATATT TGATGGGCTT TCTAGTAAAT
- 661 ACAATATAAG TTATTGGGCT TAGTTTAAAT AAGCCCATGT TGGAAATATT
- 611 TGACACATGT CTTGGCTACT AGTGCTAAAC ATGCAACCGA ACAGTTGTCG
- 561 AGACAAGTCG CAGCATATAC AATGGATCAA ACACGCCTAG TGTCGCCGCG
- 511 TCTCGCTCAT GTGTCACCTT GTTTCCTCGT TTTTTTTTAA TTTTTCATAA
- 461 GTTCTTTTGT TTTATCTTCA ATACAAATTT TTGGCTGTAT CTTGCAAACT
- 411 CTTCGATCAT ATCGCCAATA TACGTGAACA CTGGTGATCT AATTTGTTGT
- 361 GTTAATTGTT AAATTTAGAT TCTATTCTCC GGTTTAAAAG TGAATTATAT
- 311 GTATCATGGT TAAAACATTG TAAGTAAGAT GATAATAAAA TGATAAATTT
- 261 AGTTGATGGA TAACGTGAAG CAAAAAATGA GATAGATACA TTTGATTTTG
- 211 TCGTATTTTG ACATATGCGG AGAGTGAGCT ACGCGCATGA AGATCAAGAG
- 161 ACACTTGCTC GAGCTCACAG AGTGACGTGT AAAAAGCTTA GACTGAAGTC
- 111 CCCATGCAAA CCTAATCCTA CGTGGCTCAA ACCACGAGCT CACTTGACAA
- 61 TATATAAACT CCTCCTAAGT CCCGTTCTCT TCATCCATCT CTCACAACAA
- 11 ACAAAAAG -4

- 3 AAAATG

Figure 1

Promoter 03

-1148 CAAGAGTGTA AAACGTACCG ATCAAATGTC TTTATAAAAA AAACGTGTTG
-1098 ATGTTGTTCT GTGAATACAA TTAGTTCTGG TTAACAGCTG GTCGACCATT
-1048 TTCTGATGAG AATTTATGTA AGGCCATTGC TCTGGTGTTG AGAAGGTTTA
- 998 GTTTGGTTCA AGCTAACCGT GGTTAGAAAG TTAGAATATA ATGTGTTTCT
- 948 TGATCAGTGA TATCGATCGG ATTTGTATTA TTCATATTGT TTACTCTTTG
- 898 AGTAATTCAT AGTGGTAACT CTTTTTTTTT TTTTTTTTTT TTCATATTGG
- 848 TAACTCTTTG AAATGAAAAA CATAGCTAAG AATTGCTAGC TTTGATTTAG
- 798 TCGAGACGTA CGAACTCTCG ATTTTGGTTT TTGATTTGTT GGTGTAAAAC
- 748 TCTCGATATT CATAACTCGT AAGATTTTGT ACGTATCATC TTCTTATTCT
- 698 CTTCATCGCT CTGTTTTCAA TTTTATGTCA AAACATGGTT TTGGTAATTT
- 648 CTTTTACTCC TACTTCACGG TTTGAGTTAT AATTTTTTTG GTAAACCCTT
- 598 AACCACGAGT TTTGATGTAT TTTGACACCT CTAATTATGT GTGTATACGT
- 548 ACACATATAA TTCGGTATTT TCTTAACATA TATATCCCTC ATAAAAATTT
- 498 CTTACATGCA TTGTTCGTGA GTGACCCGTT AATATATATA TTGATAGATA
- 448 CTCTTATAAA ATTATATTCT AAATTTCAGA TTAAGCTGGC ACAACTATAT
- 398 TTCCAACATC ACTAGCTACC ATCAAAAGAT TGACTTCTCA TCTTACTCGA
- 348 TTGAAACCAA ATTAACATAG GGTTTTTATT TAAATAAAAG TTTAACCTTC
- 298 TTTTTAAAAA ATTGTTCATA GTGTCATGTC AGAACAAGAG CTACAAATCA
- 248 CACATAGCAT GCATAAGCGG AGCTATGATG AGTGGTATTG TTTTGTTCGT
- 198 CACTTGTCAC TCTTTTCCAA CACATAATCC CGACAACAAC GTAAGAGCAT
- 148 CTCTCTCTCT CCACACACAC TCATGCATGC ATGCATTCTT ACACGTGATT
- 98 GCCATGCAAA TCTCCTTTCT CACCTATAAA TACAAACCAA CCCTTCACTA
- 48 CACTCTTCAC TCAAACCAAA ACAAGAAAAC ATACACAAAT AGCAAAAC -1

1 ATGGCTA

Figure 2

Promoter 04

-1037 CAAACCATTG TTTACACGTC AATTTGAATT GCGTCAAATA TTCGACTGGA
- 987 ATCCTACAAC ATATTTCTTC TATTATATCA ATAGGAAGCA ACGAACGTTC
- 937 ACATGAAGCC ATGCAAAAAC AAATTGAGAA AAAAAATCAG AAAATTTATG
- 887 ACAAGTGGTC TTGCTTCTTA TACTACGTCG TGAATGGATG GTAATAAACA
- 837 ATTAAATGTT ACCTCTAGTT TTTTTTTTTT GAGAGAATGG TTTTTATCCG
- 787 TATATGGCTT ATTACAAGTT TCCTCCTTTT TCGAGTTTGG TTTGAGGTCT
- 737 ATATTGAAGA TGAGATACTA AAAATTGAGG TAAATTCTTT AGTGTGAAGG
- 687 AAAATTAGTA AATACGATAC GTTTGGAATT GTTTACTACT AAAAAAAAAA
- 637 TTGTTTTAGA CCAAGCCAGT CCGACAAAAA GGCGTGTGAA TCATAAGAAG
- 587 TATCACATGA TGCTAGACAT AAAAGATTTT TCAAACATGA CAAAACAAAT
- 537 TGTGAGTGTC TTAGTCATGC CATTTGAAGT AGAACGAAAC TTAGTGATGA
- 487 GACACGTAAC ATCAGTGAGA ATCAAGATCT AACTTCGGAC TTATCGTACG
- 437 TACCACGTCC ACCTAAGTGT TATCCATATC TACTACATGT CTATCTTCAT
- 387 TCAATTTTTT TTTTGCATTA ACTTGTAAAC ATAGTGCATA ATAATTAGAA
- 337 TCAAGATTTG AATCCAATTC GCTTACTAAA TCCTAAATGT TAAAAGCATA
- 287 CATGTTTTTC AAATCCTACT TTTAGGTGCT AAGTTTTTTT TCTAAGGTAG
- 237 TTAGAGATTG TTAGATTTTA TATCATTGAA CTGATCATCA GTCTCTATAC
- 187 TAACTTCTAG ATCTCATTGA ATGTTTACTC AATTTTTTTT AATTTTTTGT
- 137 TTGGATAATC GTCTGCTCGT GGTTTTGATG CGTACGAACA CTCGTCACCA
- 87 TGCATGTCAA GCTCTCCTTC CTATATAAAC TAAAACCACC CATTATTGTC
- 37 CTCAAAAACA AACACATCAA CAAAACAACA AG -6

- 5 AAAAAATG

Figure 3

Promoter 06

-1413 CTAAACGAGT AAAGTTTAGC ACGATTGAGA CCACACTGAC CCATAGCAGT

-1363 CCAATGAGCT ACGGAAGGCC TAGGGCTTGA GGCTTGATGA GCGCGTGGTG

-1313 GAATAGCGTT TGAATCTAAA GTTCGGTTTG GTACGACTTG TAATATGAAA

-1263 TAATAATGTA CAAAGAAGTT CTACGCTTAA GGGAACTGTT TTGTTTTGAG

-1213 CTTTGTATTA GGACGTCTAG TGTACAACAA CGAACGTCGT GTATAAGCGA

-1163 TCGTTGACTC TGCACATGTA ACTCTTTCCT GAATAAAAAA TCTTTAAGTC

-1113 TTTAATTTCT ACATCTTTTA GGATTATATA AACGTTACTA TATAAATAAA

-1063 AAAGAAAAAA AAATCAGTTC ACTAACATGC GAGACTTTGG GCTAAATATA

-1013 GTGATTCCAA AGAAAATGAG TTATAATATT AATTAATATA AAGCTCATTT

- 963 TCTTTGGAAT ATCGTTATAA GAATATTTTA ACTTGGATAT AACTGGGCTT

- 913 ACGCCATTTG CATCTCGAGG ATTTTTTGTT TTTGTTTTTG TTTTTTTAAT

- 863 ACATTCTCGC ACTTACACAC TAAAAATCAT AATGATCTTC TTAATTCTTT

- 813 AGCGGAACCA CCAATTAATC TTTTTATTAA GAACTTTATT ACTTATTTCA

- 763 CTTATTTGTG CATACGTGCA TTATTTTGGC AGTAACAAAT ATCGCGTTAT

- 713 ATATACTGAA ATCCGGACGC ATTAATAATA GGGATATGAT TATATGAACC

- 663 ACTATCTAGC TTTGGTAGAA ACCCAATTAT AATCAAATAA TTTACCATTA

- 613 TTGAATAAAT TAGGCTATAT AAGTTCATTA ATAGATGCTA TAGGTTTTTC

- 563 TTACAAGGCA CACATTTGAT TGTTATTTTC TTTCATATAC ACTGAATGTA

- 513 CATGTGTACA CTTGGCATAC ATGGCAAGAT TATGTGTTAC AATATAGACT

- 463 GTGCCATTGC CATGCAATGT GACTCCTGTG GCCATTTCTA TCACAATGTG

- 413 TCAATCTTGG AGTATCCGTT GTTTATCCTC TAATTTACTG ATTAATTTAT

- 363 GAACATGTAT AATTATTTAT ATCATATGAT CTCGTAAGAT ATCTTAGCAT

- 313 TTTCCACCAT ATGTTATTAG TAAATCATCT AGATGGATTG ATGTAAATAG

- 263 GAAAGTTAAA TTAACACACC AAAAAAGTAA CTGATTAAAA GCATACAACT

- 213 TAATATTCAG ATTATGGTAA CTAAATCAGT CTCATGCAAA CTCCAAAAAA

- 163 TTATACGAGT CACAACTCTT GATTTTTTTC CGGTTAAACA AAATACATAT

- 113 TTTCATTTGT ATGCAACCAG AATAAAACAC TAACTATCTC CTTTAAATAC

- 63 CATTTTCCCT ACGAGTCTAC GACGCTCTCT AAACTTCTTA TACAAAACAA

- 13 AACACACCC -5

- 4 AAATATG

Figure 4

Promoter 07

-1118 GATCCGAAAA GTAGAGTTTC GTGGATCTGA TAATTGGAGA AGAGAGAACG
-1068 AGCTGAAACC CTAAATTCGG ATAAAGTCTG CAACTTCTGT TGTTTCGGTG
-1018 GCGAGAACAA AAATAATGAG AGGAAGAGGA AAATATCGTC GTTTTTGTCT
- 968 CACAGTCTCT TTAGCAGCTT TTCTTTAGAT ATTTATTTTA TTTTTTCCAT
- 918 GGATAGAGAG AGCTAGGCAT TCCGGTTATT TGGAGATTTT GGAATTTCAA
- 868 TTTTGCGGTT TGGTATTTTA TTTTATTTTA TCAATTTGAA CGAAACAGAG
- 818 CTTTGTTTTG GTTACGATGC GGTGGATTTT GGTTCGGTTT AGAGTGATAT
- 768 ATATTTGGTA CCAAATTAAA CCAAGATTCG TTTTCGGTAA AAACAAAATT
- 718 TGATTTTTAA GCATTTTTGG AAAAATTAGT GTTATATATA TGAGATTTCT
- 668 TAATCAAAAT CTCACTTTTA TCCGATTTAG TGGTAGTTCA TAAAGTGGTT
- 618 TCATGTATAT GATACCTGAA TAACCAACAT ATGTATTTTA AGAGACACTT
- 568 GGAATAATAA TTCTAAATAT CCTAACTACT CGTGTCCGTA TGTTTTGTCA
- 518 CGGTGAAACG TGAGAGGACT AGTTTTTGTC ACCCGTCCAT AACATTCTTA
- 468 GACATACATT ACTTTGGGAG TGAAAAACAT TAAGCTTATC TTTATCCATA
- 418 TATTGTCTTA CCATCAATAG ACAATATCCA ATGGACCGGT GACCTGCGTG
- 368 TATAAGTAAT TTTTCAAGAT GCTAAAACTT TTATGTATTT CAGAATTAAC
- 318 CTCCAAAAAC ATTTATTGAC ACACTACTAC TCTTTCCGTA TTGACTCTCA
- 268 ACTAGTCATT TCAAAATAAT TGACATGTCA GAACATGAGT TACACATGGT
- 218 TGCATATTGC AAGTAGACGC GGAAACTTGT CACTTCCTTT ACATTTGAGT
- 168 TTCCAACACC TAATCACGAC AACAATCATA TAGCTCTCGC ATACAAACAA
- 118 ACATATGCAT GTATTCTTAC ACGTGAACTC CATGCAAGTC TCTTTTCTCA
- 68 CCTATAAATA CCAACCACAC CTTCACCACA TTCTTCACTC GAACCAAAAC
- 18 ATACACACAT AG -7

- 6 CAAAAAATG

Figure 5

Promoter 09

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- 975 TCAGAAAGAG AAGTGAGCTA CCTGCAGTGT CCTCTGTTTT GTCGATGAAG
- 925 GATTTTTAGA TTGGTATGTG ATGAAGTACA ACGAGCTGAT GCCTGCGTTG
- 875 ATGGCTATCT TCACCAAAAG TCGTGTTTGT TATGAAGCAC AACGAGCTGG
- 825 TGCCTACGTT GATGGCTATA TTCACCAAAG GTCGTGTTTC ATAGATCAGA
- 775 AGGCACACCT ACAACAATGA GCAGTGCCAA GGTTTGTTCT TATTTTGTTG
- 725 TTGTCAGTTT TAGATTTCTA GATGAATCTT ATGATGTGAT AATGGAAAAA
- 675 CGAAAGAAAA GCTTTTGTTA AAGTATCTAT GAGTGATATC ATGATATGTC
- 625 AAAAATGTTG CATGGATACA TTGATTCTTT AGTACTTGTT ACGAGCTGCT
- 575 AAGAGAGTCG TGTCAAGTTC AATACTTTTC CTTGTCATTT AACATAATTG
- 525 CTTGTCTGTT TGGATTCTAT TGTGCGGAAG TTATGATTTA TATTTTCAGA
- 475 TTCATATTTT CAATTAGGAA GCTTTAGTTG GAATCAAAGT GGATGACCCT
- 425 GATTGAGGAT TTTAATGATC GTTGTGAGAA CCTTTCTTGT AGTTAGTTGG
- 375 TGGATTGTAA AAAAATTATA TGTATTTAAC TCTTGATTGA GAGTCAGAAG
- 325 TTGGAAAAAT GAATTAAGAG GTTTTCGAAT AAGAGATCAC AGTTATAGTA
- 275 TAGTATTAAT TGGATATCAC AATCTATTCA TAATATTAGC TAGTTAGATA
- 225 AAATTGTGTT TGATCTTGGC AAGAGGTGTT AAAATAGTAT CATGTTGACA
- 175 TGTTGGTATG ACTATTAGTC GTAATTTAAG CTTATGTATA TTTCTTGTAA
- 125 GAAATGTTCA TGTATCATAA TAAATACAAG TGTATCGAGT TTTTGTATAT
-  75 ATAGAGGTCT ATGATTTGGG AAGAAGAACA CAACATAACT CACCACAAAC
-  25 ACAATCTAAT CCAAAAAATC AAAAG -1

    1 ATGAAT
```

Figure 6

Promoter 13

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-1121 TGACACGCAA CAACCAAAGC CAAAAGGGTG CGTTACCATT AATTCAGGGA
-1071 AAGCGAAATA AACCCAAATC TCTCTTCTAA CGAAGTAACA ACTCACCCAC
-1021 TTCTCACATT GATTCACTCC TTTCCAGTTT TTACATATAG CCTTCGTTCA
- 971 TCAATCACCT TAAGCAAATT GCAATCACAA AAAAAAAAAA GTACAGTACT
- 921 TAGCAAAATT TTAAGTTTTT GTTATTTCCA CGGCAACTTA GCAAATATGC
- 871 ACCACATATT GACATTAGCT AATATACAAC ACATGTTTTT TTAGAAATGT
- 821 ACAAGCATTA ACAAATATCC AACACAAAAT GACATGATCG TAGATGATTA
- 771 AGATAATTCG ATCCCTATAA CTAATAGTTT CCAAAACTTC TGCTGACTTT
- 721 TCTCTCGACA GCGATGGTAA GAAGAAGGTA CAAAGTTTTG AAGCCCGAAT
- 671 ATAACAAAAG GACAGAAAGC TTTTAGTTTT CTAGATAAGA TCTTAGCTTT
- 621 GGTCACGTAA AAAAAATTAA AAGTGAATTG GTTAACAATA TAGGAGTACT
- 571 TTGTATCCAA AGGTCATTGC AATAAATAAA CACTTAAGTA CTCTGTAGTC
- 521 ACACATCTCT AGGAGCTTAA TATTGGATAA TCGCTTGTAG ACTTGTATTA
- 471 AAATATTTAG TAGGTCAAAT CCCTATCTTC TACAGTTTCT ACTCTCGTCC
- 421 GTACAGACTA CAGACACTAT GCTATAGTTT TGTGTTGAAT TCTACAAAGT
- 371 ACAAATTCTT CTTTCGGTGC CAATAACAAA TAAACACAAT TCTCAAATTA
- 321 CATTTGTCTA AATTTTTATT TGATTCGGTA TAAATGTAAC GCTATGTTGG
- 271 GAATCATATG ATAAATCCAG ATTAAGACTT CTTATTTAAT TTATTTTTGT
- 221 ATATATAAAA TATAATATCC AACCATAAAG TTTTTTTACC GATCGATGAT
- 171 AATGTGAATC CAAATATTTT AACAGGATGA TAAATAATTG ATGTGGCTTT
- 121 TATAACCGCA GCAATTCTGG CGTGACTCTC TCCGCAGCAT TTATTTTTCT
-  71 CTCTATAAAT TAAAAACATT ACTTACTCTT TCTCTCTTCC ACTTAACTCA
-  21 TATCAACCTT CGCCGGA -5

-   4 AATAATG
```

Figure 7

Promoter 14

-1056 ATCTCTGCAA ATCAAACCTT ATTATTAAGC TACATTTACA TAGTGTCCTT
-1006 ATAATTCTCA TGACATAGCA ACATTATTAA ACGACAACTT TCTAGCTTCA
- 956 TTTAAAATGG AAAATCACAT AACACTCACA TTAACTATAC TAACATAACA
- 906 CTCACATTAC CGACTAGCAT ATAAATGGAT ATTGATATAA CAATAATCCC
- 856 CCAAATTTAT GTCTATTTTG TTCATTATGC AAATGTCCCA AAATGATATA
- 806 TCTTGGAAAG TACTAACCGG AGACGAGGGT CGAGGTATAG AAGTGATTTG
- 756 GTCGAACCGA AATGAGGAAC CCGGGTTTGG ACACCAGGAG CATTTTGGTA
- 706 ATCATCCAAA TCAGGGTCAT AGTACAACAT CATTCGATCG CTGAAGCACC
- 656 TGGTGAAGGG AGACAATAAC ACTGCTGCAT CGAACCATAG CCTAAACCAT
- 606 CCACCACTCT TCTTATGAAT CGGATATAAC CAGCTGCTAC ACCAGACACT
- 556 ACTTGGCTTG TATTCTCTGT CCAGCCGTAC CTCTAGCTGG TTACCTCCGT
- 506 TTCCTGGAAC CAGAATCAAA GGGTACACGT TGCTACCCAC AGCTTGACAC
- 456 ATCGAGGTCA TCGTCACCAC AACGAGTATC GCTATGACTA CCGAATAATG
- 406 TGAAGATATT TTTTTCATTT TCGTTCTAAG AAACAGACTC TCATGGTCAT
- 356 GGATCTATGC AGAAAGCTGG AGATTTGAAG AAAAAGGTCC ATTGAATTTG
- 306 AAAAACAGAG TAGTATCTTA AAACGTAAGG CTTAAGATAA GTAGTATATG
- 256 GTGGATATGG AACCCGCGTA ATCATCTAGA GGCTCTACAA ATATTTATTT
- 206 TGTATTTCCT TCTTATTTTG TATTTGCCTA CGTGGCATTA TACAACGTAT
- 156 TTAACTTGAA ACCAGATTTA TGGCCCAATG GGTCGGGTCG ACCCGACCGA
- 106 TTTTAAACTG CGCTCCTAAC TAAAAAAAAG TCAAAACCCT TTGAAAAACC
- 56 TAAAAACGCA ATTTGCTTCG TCGTCTCTCA TCTCTTTCTC TTTCTCCG -9

- 8 TCGCCACCATG

Figure 8

Promoter 15-2

-1074 GTAAGTCGTT CTCTAATCTT CCATGCCAAT TTGCTCGGTT AAAACCAGAC
-1024 TGGTTGGACT GAAAAATCGG TTTTAATTAA TTGAGTTGTG CTTATGAGGT
- 974 CTATTGGTTT ATTTTTAAAA TCCTTTGTAG ATTAGGAGAG TACCAACAAG
- 924 AGCGAAAGAC ATCACTAAAC ACGAAGAGTG AAAGTGGAAA AAGAGAACTA
- 874 TCAAGACTTG ACTCGAAGAC CGGATTGTAC CCGGATGATT CGAAACAGGG
- 824 CGGTGCTGGT GCTGGTGCTG GTGGTTGGCT TTCTTGTTGT CTCTGTTTTT
- 774 CGGTGAAAAA TTGAGGTTAT TACTCTTTGT CATGTCAATT ATTTAGGTCA
- 724 TAGCTGTCCA AGAGACGCGA GACATTAGAC AAGGTAATTA CCGATTGTAT
- 674 CCTATATATT CCTATGTAAC GAAATTCAGA TACTACGTAA TCTTAATGTG
- 624 TCGATGGAAT GAAAAAATAA AGTATTCTGT AAATATTTTC TATATATTAT
- 574 TTAGCATATA TACGCTTTAT AAATTATAAA TTTGGTCCCT CCCAAATACA
- 524 TGAAAACAAT GTAGTGATAA AAAAAAAACA AATTCTGTAT ATATGCTATT
- 474 TTTATAACAT AACAAGCATT TTTCTTAGTC GGTTAAAATT TCAAGTGTTT
- 424 AATACTTTTA TATAATTATG AACGTAAGTT ATAATCTATG TTTTTTTTGG
- 374 TCAGTCCATT ATTGATTATT CCATTCACAC TATATGCAAC CTATATTCTT
- 324 CCTATGAAAC TTTTGATCGT GTGTTAAATA ATAATACAAA TTTGATTTCA
- 274 TCTAATAGGT GGGTGGGGAC TCTCTAATTA CGTTCTTTGA CATCTACTCA
- 224 TCAACATTTG GCTAATCTTT CTAAAGGAAT TCCATCTACC GGTCATTTTT
- 174 GTTTAAATGC TCTCTTGTAA CTAAAAGTCC GTACCAAACT TGTGTAATTT
- 124 CATTAAACAT TAATTATTTA GTCCATTCCA TGTCAAATAT GACTTCTATG
- 74 CTCTTGTCCT ATAAATTTTA AGCAATGAG GATTCACCAA GTATACATGC
- 24 ATAACAAATT AAGAGCGAG -6

- 5 CAATAATG

Figure 9

Promoter 16

```
-1044 GTGAGAAAAT TCATGAGCAC TCTTAGAAAT GTAAATAGTT TGATTTGAAG
- 994 AAATGTGGTT TTTAAGAAGA TAATTGCAAA ACTCAGAAAG GATTTCACAA
- 944 AAAACAATTC GTGAAATCTT TCCTGAATTT CGTAAAATCC TTTCTAAATT
- 894 TTAGAAAATT ATTATTTGAA TGATTTTACG AAATTTCGGA AAGAATCTAT
- 844 AAAATTCAGG AAAGATATCA TAAAATTTAT GAAGAGTTAT ACACAACAAA
- 794 AAGAAATTTT TGAATTTCAT GAAATCCTTC GTAATTGCTT ACATTCCTTC
- 744 CTAAATTTTG TAAAATTCTT CCTGGATTTT CTTTTGCGAG AAAATAGGGG
- 694 CATATATTTT TTACGGGAAA TTTTTTGACG AAAACTTATT TTGGCGGAAA
- 644 AAATTGTCAG GAATTTTTGG TAATGAATAT GTGTATTTTT TTAATTGTTA
- 594 ATTTTAATAA TAAAATAAAA TAGTTATCTG AATGTTATTT ATGTCAAAAA
- 544 AAAATATGAA TGCTATTTTT GTCTTAAAAA CTTAAAATTG TACTATTTGA
- 494 AGGAATTTCA TTTTATTTTA TTAATGTGAT TAGATTTATA ATTAAATATA
- 444 ATTAAATGAT TGTAAATACT AACTTAAATT CTTATTTATA AACATAAAGT
- 394 AATATTTAAT TTTCTTTAAT TAAAAATACA TATTTTATTT TCATAATTTA
- 344 TTTTGCTTTT TTTTTTTTTT AGTTTTGATT TATTTTTAAA CATATAATAT
- 294 GAGTATATGA CTATATGACA TAGCATATTG GTTTATTTTG ATTAGATAGA
- 244 AAAAGAGACG GGTGAATAAA AGGGTTTAAT ACTATGGTGA ACCCAAGTAT
- 194 ATATCGTCCA TAACAAAAAC ACTATATAAT TGAGGTTTGT AGATTGTGCA
- 144 AACACGTGTG GGCATATCAG CTTGTAGGAT TGCCACATAC ATTATCATGA
-  94 GAAGCTTCCA CCAGAATAAA GCAAAACAAA AAACTCCGAA AGCGGAGAGA
-  44 ACAAGGAAAA CTGAAAAACC ATTGTGAAGT ATAGTCCTTG ATGC -1

     1 ATGGATT
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Figure 10

Promoter 17

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-1141 CAAACGAGGC TCCAAATTCA TATTCGGCCT GCATACTTTT GCCCTGGCCC
-1091 GGTTTTTTTT TTTCTTTTTT TCGGTGTTTC ATAATACATC AGCTTCCATA
-1041 ACTGGAGCAA CCGTTATAGA AAGACATGTA TAAGAACCCC AAAAAAACAG
- 991 GTACGTCAAA AGAGGAAATT CTCATAACAT ACACAATATG CTCCTAATCA
- 941 GCCATCGTGT TGTGCTGATC TCCTAGGTGA CATTATGTAT ATCTGTTTGA
- 891 TATTTCTTTA ACACAACATG TTATCAGTTA CCCATCAAAA CGTAGTCAGC
- 841 TTGAGGTCTT CCAAAAAAAT CCACACTAGA CCTTCCTTCA TCACTTCAAC
- 791 AGACTTCAAA CTTCTATCCC AAAAGGAAAA AACTAAATAA GTTGAAAGGA
- 741 ATGGTCGAAG GCATGGGGAG ACACCTAATA CGGCAGCTAG ACTAATCCGG
- 691 TGGATTGATA AGCAAACTCG AAACACTCTT TCCTCTATCA GATTATTGGG
- 641 GGATAGGAGA TATGACAAAA GACTGCAAAT GTGGTTTGCT TCTAGAAGTT
- 591 AAGAGCTTCC GGGATTTTGT TTTTTATTTT TTCAGTGTTG TAACAAATTT
- 541 AAATTCTGTC GCACTTGTCG TAACAACGAT ATTTTTTCTT TGAATATAAT
- 491 TTAACATTAA ATTAAAAAGA AAAACTAAAT AAATTATTTT GAAGTTAATA
- 441 TATTATGTTA TTATCTTTGG TTTGCAATAA ATAGATCGAG TCAAGGTCGT
- 391 TATATGACCA TTGTTTAGTT ACGACGCTAC TTCATACTTG GAATCTAAGG
- 341 AGAAAAAATG TAACATAGTT CTCAGTACTT AATCACATAG TTCTCAGTTC
- 291 TTAATCACTT TATTGTTAAA ACTTTTCATC GAATAATTAA TGATTTGATC
- 241 TCCAATCTCA ATTAATTATA TATTTCTAAA GCCAAAAGAG ATAATGAAAG
- 191 GAGAGGTGGT AGAAAGAAAA CGTTAATGTA TCAAACTCTA ATAAAAGAAA
- 141 CTGCGTGTAT AGACACGAAG GCTCCGATCT TTTGCATGTC TCGCACGTGT
-  91 CGTCCTCTTT CTTCCTACTT AACACATATA TGCATGCACC CTTCTTAGAA
-  41 AAGTAGCAAA ACATTGTGAA TCATCGGAGA GAGTGGGAAA C -1

   1 ATGGAGA
```

Figure 11

Promoter 19

-1293 CACCAAGCCT ATACAAACAT AATTTAACGC CGCCTAGTTT TGTTTATTCT
-1243 GCACGTAACA TATAAAGCTA ACAGATATGC GACAAAATAT CTATAAATTA
-1193 CATATATAAG TATATATAAT ATAAGAATGT TGGATGTATA TATTAGTAGT
-1143 TTAATCAATG AAAATATATC TTTATATCTT TATTAAAAAA ACTAAAAATG
-1093 TATCTTTATA TACATTTCGT AGTTTAAAAT CAAAATTCAA GATAGAGCGA
-1043 AAATGATTTT TTTTTTTTTA AATGAACCAA AAGTACAACA TTCCTACCTT
- 993 TATTTTTAAT AACTCGTTTA TATTCGCCAA TCAGACACAC ACATAGACTT
- 943 TTAAAATAGT AAAAGTAACT TAGCCGATTA TTTATGTAAA ATATTCGTAT
- 893 AAAATTTTTA TTAACAAATA TATTTGATTT CTCATCTTAT AACCTGTTTA
- 843 TTGATCAGAT TACACGAAAA AATAACTAAA CAGATAAATT TACTCGAACT
- 793 GCATACAATA GAGATGTATT TGTGCATGAG TGTAGCCCAA AAATGTGTAA
- 743 GGAAATAACA CCCATTGGTA GGCCGAGACA TGCCTGTACC ATGGCCGCTG
- 693 AAATAGTAGA AGAACCAAAT ACCTACCAAA GTACTCTTAA GCTAACGTTG
- 643 ACATGATTTA ATTAGATTAA CGATTGAGTA AACGACAAAT TAGCGCTTTC
- 593 GTTTTATATT AAAGACGCAC GATATTTAAA TGGCAACTAT ACATTAAAAT
- 543 TATATAAAAT ATATAACTAT AACCAATTTG ATAAATGAGA AAAATGTACG
- 493 ATATGTCGTA CCACTCCATC CTGACTATGA CTTATGGAGG AAGTCAATGC
- 443 TTATCAACTA CTTGCTTATC AATATCCTAT TTATCACTAT CAGTTTTTCT
- 393 CTTTTCTATA CATATATTAT TTCCTATAGA TCATGTTGGT CATAATGTAA
- 343 TCAACTTAAA ATTTAAGATC TACTAGTTTG TGTTGAAGTA TAACTGTATA
- 293 AGCCTAAATT CGAACGTTAG TCTGACTTAA TAGTTAATTC CATTTTGTTT
- 243 TGGGTAAATG TTTCAGTTTC ACTGCTGTTT GGAAAATCTT TGGACAGATA
- 193 TTGAGATTGG GCTTATAATA TTTATTATTG GGCCTTAATT TAAGAGCCCT
- 143 TTTATAGGCA GATACAAAAA CGACGGCGTT TAACTCATCC GCTCAGCGAC
- 93 TTCCACATAG CCGTTAAAAC GATGATAATA AACCCAATCC GGTTCATCTC
- 43 CAACAGAAGA ACGTAATAAC TGATGCTTGT CTTCAAGTCA AC -2

- 1 CATGGAGT

Figure 12

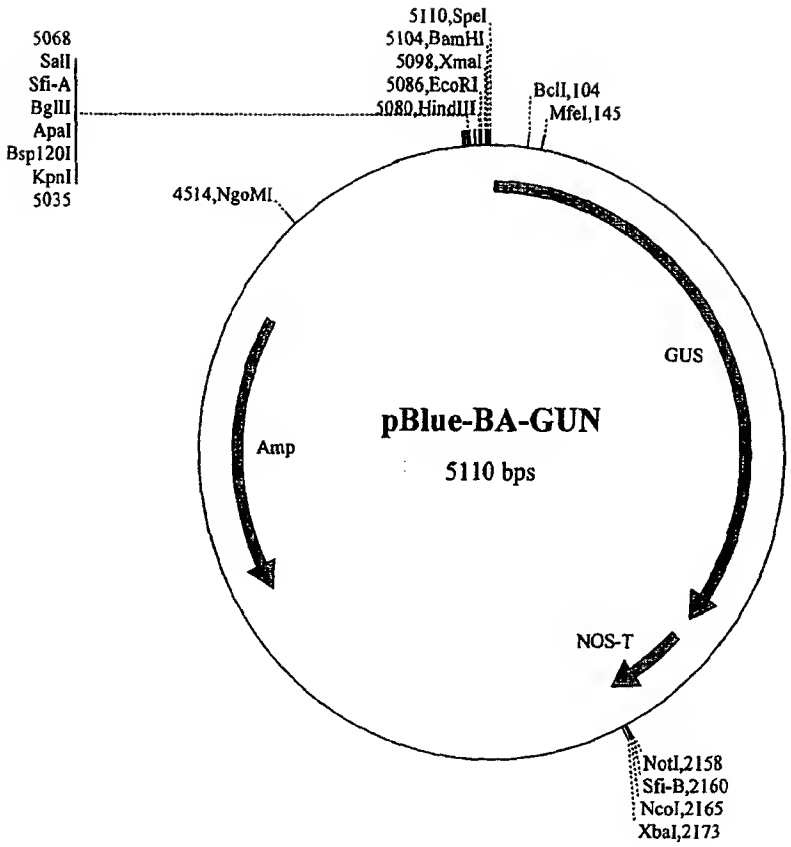

5110,SpeI
5104,BamHI
5098,XmaI
5086,EcoRI
5080,HindIII
5068
SalI
Sfi-A
BglII
ApaI
Bsp120I
KpnI
5035
BclI,104
MfeI,145
4514,NgoMI
GUS
pBlue-BA-GUN
5110 bps
Amp
NOS-T
NotI,2158
Sfi-B,2160
NcoI,2165
XbaI,2173

Figure 13

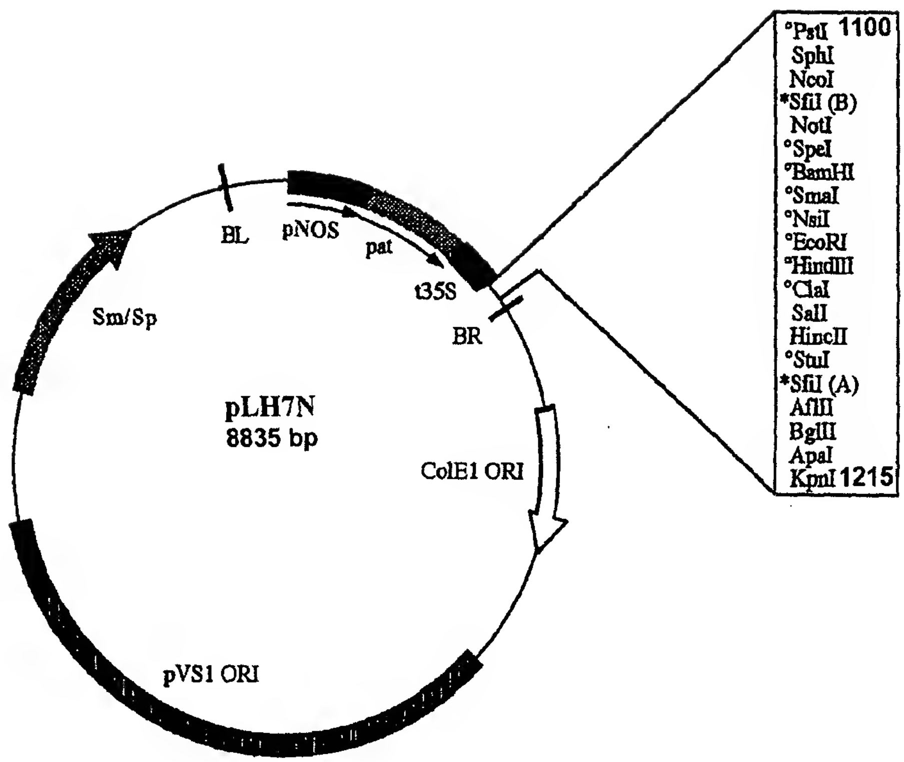


Figure 14

Promoter 6 :

GATCTCTCCCGAAGAAG

CTAAACGAGTAAAGTTTAGCACGATTGAGACCACACTGACCCATAGCAGTCCAATGAGC
TACGGAAGGCCTAGGGCTTGAGGCTTGATGAGCGCGTGGTGGAATAGCGTTTGAATCTA
AAGTTCGGTTTGGTACGACTTGTAATATGAAATAATAATGTACAAAGAAGTTCTACGCT
TAAGGGAACTGTTTTGTTTTGAGCTTTGTATTAGGACGTCTAGTGTACAACAACGAACG
TCGTGTATAAGCGATCGTTGACTCTGCACATGTAACTCTTTCCTGAATAAAAAATCTTT
AAGTCTTTAATTTCTACATCTTTTAGGATTATATAAACGTTACTATATAAATAAAAAAG
AAAAAAAAATCAGTTCACTAACATGCGAGACTTTGGGCTAAATATAGTGATTCCAAAGA
AAATGAGTTATAATATTAATTAATATAAAGTTATTTCTTTGGAATATCGTTATAAGA
ATATTTTAACTTGGATATAACTGGGCTTACGCCATTTGCATCTCGAGGATTTTTTGTTT
TTGTTTTTGTTTTTTTAATACATTCTCGCACTTACACACTAAAAATCATAATGATCTTC
TTAATTCTTTAGCGGAACCACCAATTAATCTTTTTATTAAGAACTTTATTACTTATTTC
ACTTATTTGTGCATACGTGCATTATTTTGGCAGTAACAAATATCGCGTTATATATACTG
AAATCCGGACGCATTAATAATAGGGATATGATTATATGAACCACTATCTAGCTTTGGTA
GAAACCCAATTATAATCAAATAATTTACCATTATTGAATAAATTAGGCTATATAAGTTC
ATTAATAGATGCTATAGGTTTTTCTTACAAGGCACACATTTGATTGTTATTTTCTTTCA
TATACACTGAATGTACATGTGTACACTTGGCATACATGGCAAGATTATGTGTTACAATA
TAGACTGTGCCATTGCCATGCAATGTGACTCCTGTGGCCATTTCTATCACAATGTGTCA
ATCTTGGAGTATCCGTTGTTTATCCTCTAATTTACTGATTAATTTATGAACATGTATAA
TTATTTATATCATATGATCTCGTAAGATATCTTAGCATTTTCCACCATATGTTATTAGT
AAATCATCTAGATGGATTGATGTAAATAGGAAAGTTAAATTAACACACCAAAAAAGTAA
CTGATTAAAAGCATACAACTTAATATTCAGATTATGGTAACTAAATCAGTCTCATGCAA
ACTCCAAAAAATTATACGAGTCACAACTCTTGATTTTTTTCCGGTTAAACAAAATACAT
ATTTTCATTTGTATGCAACCAGAATAAAACACTAACTATCTCCTTTAAATACCATTTTC
CCTACGAGTCTACGACGCTCTCTAAACTTCTTATACAAAACAAAACACACCC

AAATATG

```
Query: 1  ATTCCAAAGAAAATGAGTTATAATATTAATTAATATAA-AGCTCATTTTCTTTGGAAT 57
           ||||||||||||||||| | || |||||||||||||| | | |||||||||||||||||
Sbjct: 57 ATTCCAAAGAAAATGAGCTTTA-TATTAATTAATATTATAACTCATTTTCTTTGGAAT 1
```

Figure 15

Promoter 14 :

CATCTCTGCAAATCAAACCTTATTATTAAGCTACATTTACATAGTGTCCTTATAATTCT
CATGACATAGCAACATTATTAAACGACAACTTTCTAGCTTCATTTAAAATGGAAAATCA
CATAACACTCACATTAACTATACTAACATAACACTCACATTACCGACTAGCATATAAAT
GGATATTGATATAACAATAATCCCCCAAATTTATGTCTATTTTGTTCATTATGCAAATG
TCCCAAAATGATATATCTTGGAAAGTACTAACCGGAGACGAGGGTCGAGGTATAGAAGT
GATTTGGTCGAACCGAAATGAGGAACCCGGGTTTGGACACCAGGAGCATTTTGGTAATC
ATCCAAATCAGGGTCATAGTACAACATCATTCGATCGCTGAAGCACCTGGTGAAGGGAG
ACAATAACACTGCTGCATCGAACCATAGCCTAAACCATCCACCACTCTTCTTATGAATC
GGATATAACCAGCTGCTACACCAGACACTACTTGGCTTGTATTCTCTGTCCAGCCGTAC
CTCTAGCTGGTTACCTCCGTTTCCTGGAACCAGAATCAAAGGGTACACGTTGCTACCCA
CAGCTTGACACATCGAGGTCATCGTCACCACAACGAGTATCGCTATGACTACCGAATAA
TGTGAAGATATTTTTTTCATTTTCGTTCTAAGAAACAGACTCTCATGGTCATGGATCTA
TGCAGAAAGCTGGAGATTTGAAGAAAAAGGTCCATTGAATTTGAAAAACAGAGTAGTAT
CTTAAAACGTAAGGCTTAAGATAAGTAGTATATGGTGGATATGGAACCCGCGTAATCAT
CTAGAGGCTCTACAAATATTTATTTTGTATTTCCTTCTTATTTTGTATTTGCCTACGTG
GCATTATACAACGTATTTAACTTGAAACCAGATTTATGGCCCAATGGGTCGGGTCGACC
CGACCGATTTTAAACTGCGCTCCTAACTAAAAAAAAGTCAAAACCCTTTGAAAAACCTA
AAAACGCAATTTGCTTCGTCGTCTCTCATCTCTTTCTCTTTCTCCG

TCGCCACC**ATG**TTTGAGTACCGGTGCAGCTC

```
Query: 1  AATGGGTCGGGTCGACCCGACCGATT 26
          ||| |||||||||||||||||| |||
Sbjct: 26 AATCGGTCGGGTCGACCCGACCCATT 1
```

Figure 16

Promoter 16 :

AGGGACTAGGAACTTAAGAAAAACAAAGTCATCAAAAAAACAAAAAAAAAGTT

GTGAGAAAATTCATGAGCACTCTTAGAAATGTAAATAGTTTGATTTGAAGAAATGTGGT
TTTTAAGAAGATAATTGCAAAACTCAGAAAGGATTTCACAAAAAACAATTCGTGAAATC
TTTCCTGAATTTCGTAAAATCCTTTCTAAATTTTAGAAAATTATTATTTGAATGATTTT
ACGAAATTTCGGAAAGAATCTATAAAATTCAGGAAAGATATCATAAAATTTATGAAGAG
TTATACACAACAAAAAGAAATTTTTGAATTTCATGAAATCCTTCGTAATTGCTTACATT
CCTTCCTAAATTTTGTAAAATTCTTCCTGGATTTTCTTTTGCGAGAAAATAGGGGCATA
TATTTTTTACGGGAAATTTTTTGACGAAAACTTATTTTGGCGGAAAAAATTGTCAGGAA
TTTTTGGTAATGAATATGTGTATTTTTTTAATTGTTAATTTTAATAATAAAATAAAATA
GTTATCTGAATGTTATTTATGTCAAAAAAAAATATGAATGCTATTTTTGTCTTAAAAAC
TTAAAATTGTACTATTTGAAGGAATTTCATTTTATTTTATTAATGTGATTAGATTTATA
ATTAAATATAATTAAATGATTGTAAATACTAACTTAAATTCTTATTTATAAACATAAAG
TAATATTTAATTTTCTTTAATTAAAAATACATATTTTATTTTCATAATTTATTTTGCTT
TTTTTTTTTTTTAGTTTTGATTTATTTTTAAACATATAATATGAGTATATGACTATATG
ACATAGCATATTGGTTTATTTTGATTAGATAGAAAAAGAGACGGGTGAATAAAAGGGTT
TAATACTATGGTGAACCCAAGTATATATCGTCCATAACAAAAACACTATATAATTGAGG
TTTGTAGATTGTGCAAACACGTGTGGGCATATCAGCTTGTAGGATTGCCACATACATTA
TCATGAGAAGCTTCCACCAGAATAAAGCAAAACAAAAAACTCCGAAAGCGGAGAGAACA
AGGAAAACTGAAAAACCATTGTGAAGTATAGTCCTTGATGC

ATGGATTCAATCAACAAGATCATCAACTTCTTGTTTCCTCTCT

```
Query: 1   TGAAATCTTTCCTGAATTTCGTAAAATCCTTTCTAAATTTTAGAAAATTATTATTTGAAT 60
           ||| ||||||||||||||  || | || || | ||||||   ||||| |||     |||
Sbjct: 109 TGATATCTTTCCTGAATTTTATAGATTCTTTCCGAAATTTCGTAAAATCATTCAAATAAT 50


Query: 61  GATTTTACGAAATTTCGGAAAGAATCTATAAAATTCAGGAAAGATATCA 109
            |||||   |||||| | || || | ||  ||||||||||||||| |||
Sbjct: 49  AATTTTCTAAAATTTAGAAAGGATTTTACGAAATTCAGGAAAGATTTCA 1
```

Figure 17

Table 2. Selected Seed-Specific Genes

The selected ESTs and their predicted protein sequences were blasted against protein and DNA sequence databases of NCBI, to identify a possible function of each gene and its corresponding Arabidopsis genome sequence.

ID	Description based on BLAST search of EST	Expression Ratio	Clone ID	Accession Number of Genomic Clone	BLAST Alignment of EST to Genomic Sequence	
1	12S Cruciferin	49.9	M30C01	AL021749	13---283 65745---66103	
2	12S seed storage protein	78.8	M29F06	AB005239	191---399 15999---15804	
3	2S SEED STORAGE PROTEIN 3 PRECURSOR	41.5	M09C04	AL035680	8---369 32165---32525	
4	vicilin precursor	19.1	M60B08	AB022223	17---400 2559---2943	
5	similarity to vicilin (7S globulin)	17.3	M51A09	Z99708	15---328 69093---69460	327---399 69490---69563
6	12S seed storage protein	23.4	M19H03	AC003027	34---220 67515---67329	218---400 67229---67048
7	2S SEED STORAGE PROTEIN 1 PRECURSOR	60.0	M52E11	AL035680	22---380 27709---28066	
8	Unknown gene Laccase-like (diphenol oxidase)	11.6	M18A04	AB017064	24---150 66806---66680	148---371 66193---65973
9	Unknown protein Arabidopsis	37.2	M42C12	AC000375	16---399 8408---8025	
10	unknown protein	29.7	M20H04	AC004392	25---390 90414---90780	
11	Putative pyruvate kinase	69.2	M36D01	AB009055	32---374 68629---68966	
12	pyruvate dehydrogenase E1 alpha subunit	27.5	M15B07	AC007323	3---373 48490---48120	
13	Similar to nucleoid DNA-binding protein, aspartic proteinase, and pepsinogen A precursor	7.0	M42A08	AB026658	28---393 68590---68226	
14	A large hypothetical protein	8.6	M40D09	AC004557	18---393 82725---82350	
15	germin-like protein (oxalate oxidase), similar to auxin-binding protein, plant only	42.1	M31F10	AB010694	13---400 18058---17673	
16	Similar to 11beta-hydroxysteroid dehydrogenase, oxidoreductase	39.3	M13A03	AB023037	9---201 52852---52660 395---426 52096---52065	199---388 52589---52400

Figure 18a

ID	Description based on BLAST search of EST	Expres-sion Ratio	Clone ID	Accession Number of Genomic Clone	BLAST Alignment of EST to Genomic Sequence	
17	putative seed storage protein (vicilin-like)	19.0	M32C09	AC006587	23---161 14510---14372 342---400 14033---13975	158---341 14289---14106
18	Lipoxygenase-like protein	16.8	M30E03	AB022215	21---99 47943---48021	96---308 48768---48978
19	Unknown gene, some similarity to selenium-binding protein-like gene	31.8	M55E09	AC002387	26---90 73712---73648 245---400 73308---73153	89---244 72555---73400
20	Cytochrome P450-like protein	25.4	M32E09	AB007648	21---394 16931---16559	

Figure 18b

Table 3. Primers for the PCR amplification of 12 promoter regions

name	sequence	position	REs	T(°C)	Length 1	Length2
1R	CACT GGATCC **TTTTTGTTTGTTGTGAGAGATG** (SEQ ID NO: 31)	best+3	Bam	48	23	32
1F	CACT GAATTC **ACAAACATACACTCAAAATC** (SEQ ID NO: 32)	best	Eco	48	21	30
3R	CACT GGATCC **GTTTTGCTATTTGTGTATGTTTTC** (SEQ ID NO: 33)	best+0	Bam	48	24	34
3F	CACT GAATTC **AAGAGTGTAAAACGTAC** (SEQ ID NO: 34)	best	Eco	48	18	27
4R2	CACT GGATC **C TTGTTGTTTTGTTGATGTGTT** (SEQ ID NO: 35)	best+5	Bam	48	22	31
4F2	CACT GAATT **C CATTGTTTACACGTC** (SEQ ID NO: 36)	best	Eco	48	16	25
6R	CACT GGATCC **GGGTGTGTTTTGTTTTGTATAAG** (SEQ ID NO: 37)	best+4	Bam	52	23	33
6F	CACT GAATT **C TAAACGAGTAAAGTTTAGCAC** (SEQ ID NO: 38)	best	Eco	52	22	31
7R	CACT GGATC **C TATGTGTGTATGTTTTGGTTC** (SEQ ID NO: 39)	best+6	Bam	52	22	31

Figure 19a

name	sequence	position	REs	T(°C)	Length 1	Length2
7F	CACT GAATTC **GATCCGAAAAGTAGAGTTTC** (SEQ ID NO: 40)	best	Eco	52	20	30
9R2	CACT GGATC **C TTTTGATTTTTTGGATTAGATTGTGTTTGTGGT** (SEQ ID NO: 41)	nb+0	Bam	52	34	43
9F	CACT GAAT **TC AGAAAGAGAAGTGAGC** (SEQ ID NO: 42)	best	Eco	52	18	26
13R	CACT GGA **TCC GGCGAAGGTTGATATGA** (SEQ ID NO: 43)	best+4	Bam	60	20	27
13F	CACT CAAT **TG ACACGCAACAACCAAAGC** (SEQ ID NO: 44)	best	Mfe	60	20	28
14R	CACT GGATC **C GGAGAAAGAGAAAGAGAT** (SEQ ID NO: 45)	best+8	Bam	52	19	28
14F	CACT GAATT **C ATCTCTGCAAATCAAACC** (SEQ ID NO: 46)	best	Eco	52	19	28
15R	CACT GGATC **C TCGCTCTTAATTTGTTATGC** (SEQ ID NO: 47)	best+5	Bam	52	21	30
15F	CACT CAATT **G TAAGTCGTTCTCTAATCTTC** (SEQ ID NO: 48)	best	Mfe	52	21	30
16R	CACT GGATCC **GCATCAAGGACTATACTTCAC** (SEQ ID NO: 49)	best+0	Bam	56	21	31

Figure 19b

name	sequence	position	REs	T(°C)	Length 1	Length2
16F	CACT GAATTC **GTGAGAAAATTCATGAGCACTC** (SEQ ID NO: 50)	best	Eco	56	22	32
17R	CACT GGATCC **GTTTCCCACTCTCTCC** (SEQ ID NO: 51)	best+0	Bam	56	16	26
17F	CACT GAATT C **AAACGAGGCTCCAAATTC** (SEQ ID NO: 52)	best	Eco	56	19	28
19R	CACT GGATCC **GTTGACTTGAAGACAAGC** (SEQ ID NO: 53)	best+1	Bam	52	18	28
19F	CACT GAATT C **ACCAAGCCTATACAAAC** (SEQ ID NO: 54)	best	Eco	52	18	27

Position: Distance from the best position (for reverse primers, it is ATG)

REs : Restriction enzyme sites included

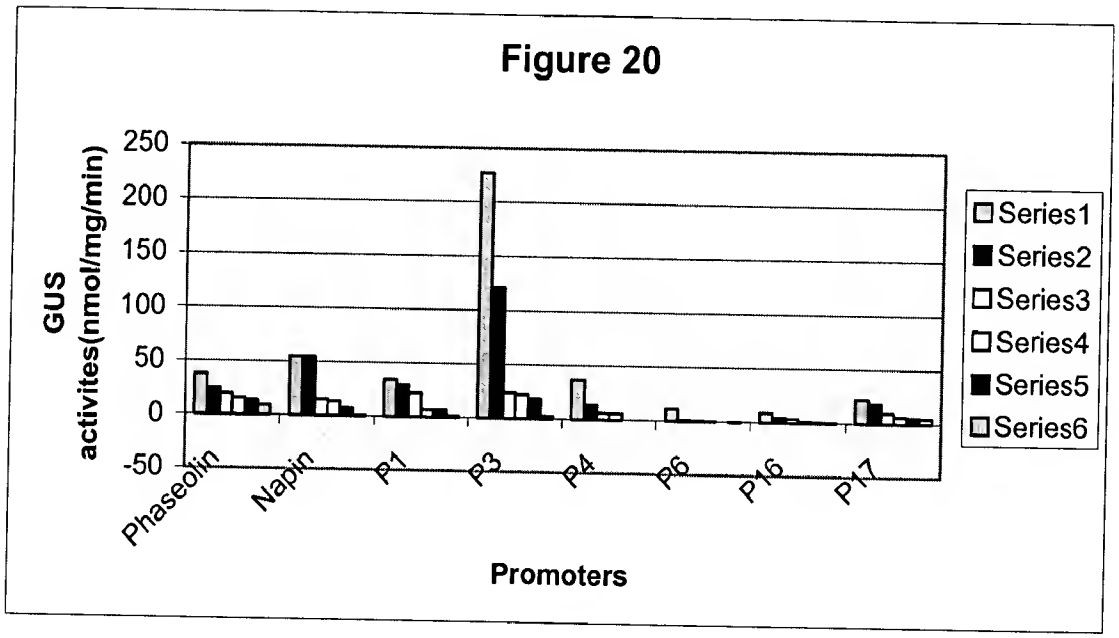
T(°C): Anealling tempeture

Length 1: Length of the sequences exist in genomic sequences

Length 2: Full length

Figure 19c

Figure 20



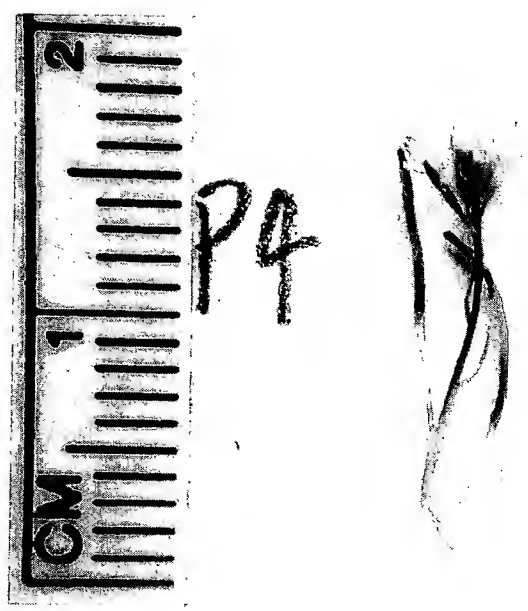
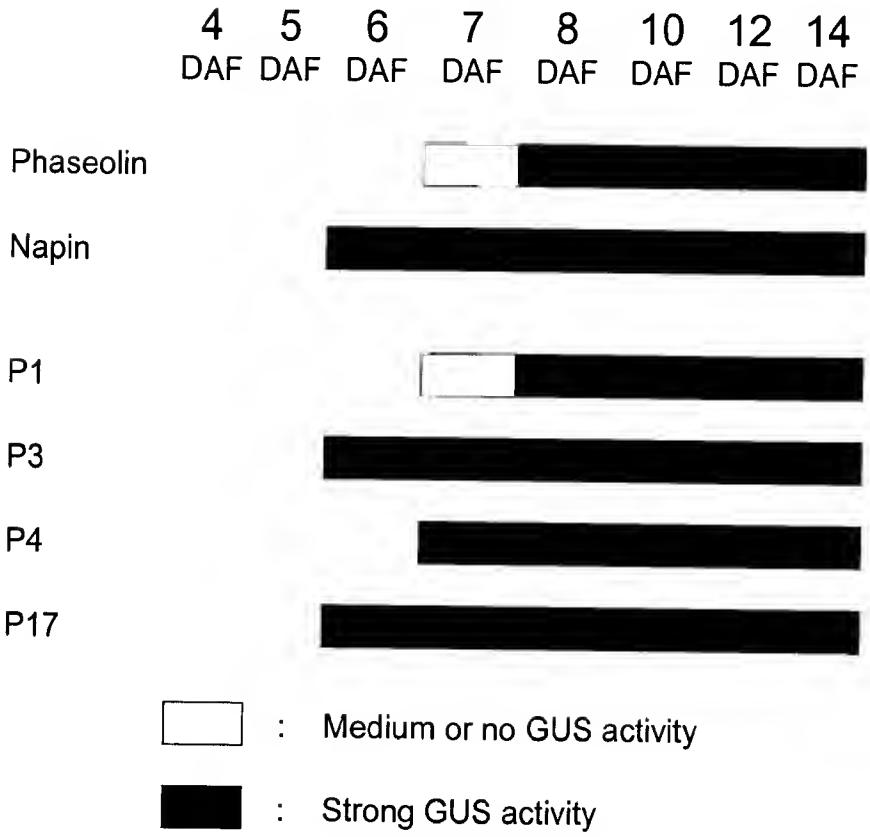


Figure 21

Figure 22


4 DAF
5 DAF
6 DAF
7 DAF
8 DAF
10 DAF
12 DAF
14 DAF
Phaseolin
Napin
P1
P3
P4
P17
: Medium or no GUS activity
: Strong GUS activity